International Journal of Infectious Diseases (2006) **10**, 188—189

ELSEVIER

INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES

http://intl.elsevierhealth.com/journals/ijid

BOOK REVIEW

Parasite Genomics Protocols
Sara Melville (Ed.), Methods in Molecular Biology, Vol. 270, Hardcover 472 pages, ISBN 1-58829-062-X (US$119.50) http://www.humanapress.com/.

There could be no more appropriate time to be dipping into a recently-published volume focussed on parasite genomics. The last few years have seen the publication of complete genome sequences for several of the major parasites of man: the big killer, *Plasmodium falciparum*, in 2002[1] and more recently, the genomes of *Cryptosporidium* species,[2,3] *Entamoeba histolytica*[4] and the 'Tri-Tryp' species, *Leishmania major*, *Trypanosoma brucei* and *Trypanosoma cruzi*.[5—7] Other parasite genome sequencing projects are nearing completion, while the 'worm' community are actively preparing for the challenges of the larger helminth genomes. The promise that this huge research investment brings to unravelling the biology of these fascinating organisms — and revealing new targets for their eradication and the prevention of human disease — has been anticipated with excitement. And already the mainstream scientific journals are adjusting to the appearance of diverse 'non-model' parasite species with unusual and fascinating biological processes. So how useful at this time is a book such as this?

Parasite Genomics Protocols aims to introduce genomic methods to a wide audience — to remove the mystique and open up the ideas and resources to anyone who can utilize them. So far, so good — the first three chapters of this book, written by some of the experts from the two major sequencing centres that have done much of the work to date (The Wellcome Trust Sanger Institute, UK and The Institute for Genomic Research, USA) provide clear and comprehensive accounts of the strategies for sequence generation and annotation, plus a very useful overview of databases and other resources. The obvious anomaly — that computer resources are essential for access to this constantly-evolving information that is here captured in print — is addressed by provision of numerous web addresses (although some of these will no doubt already be obsolete). However, for both the novice and the experienced researcher, these chapters are informative and go a long way in demystifying some of the methods and terminology associated with genome sequencing and analysis.

The remaining 21 chapters move into the protocols of the title and provide a mixed bag of methods, loosely organized into genomic and post-genomic strategies for experiments in functional parasite biology. Topics include a range of techniques for analysis of parasite DNA organization and variation and then move to methods for studying global gene expression and function. Of necessity, there are different strategies for the study of different parasites, which range from the multicellular helminths to the unicellular protozoa. Clearly, not all of these will be of interest to all readers, and some will not find a wide audience due to their specialized content.

There are, however, some extremely useful chapters here that will expertly guide researchers who want to exploit new approaches to functional genomic analysis in these complex organisms. To name just three topics from a longer list, the chapters on transfection of *Plasmodium falciparum* (Crabb et al.), gene deletion and protein tagging in *Trypanosoma brucei* (Arhin et al.) and transposon mutagenesis in *Leishmania* (Robinson et al.) are likely to attract wide readership and application.

Without doubt, there is a huge amount of useful information in this volume, contributed by experts in their respective fields, which will draw the interest of many. Parasite Genomic Protocols will be a useful addition to my library and I suspect that new students and postdocs will find much practical advice in its pages. It should be remembered, however, that the contents of this book reflect a research field in transition; it is by the application of these methods that we will ultimately transform our understanding of parasite biology. Such advances will underpin the development of new diagnostics, drugs and vaccines, goals that will take time, money and hard work to achieve.

1201-9712/$32.00
doi:10.1016/j.ijid.2005.10.003

References

1. Gardner MJ, Hall N, Fung E, White O, Berriman M, Hyman RW, et al. Genome sequence of the human malaria parasite *Plasmodium falciparum*. *Nature* 2002;**419**:498—511.
2. Abrahamsen MS, Templeton TJ, Enomoto S, Abrahante JE, Zhu G, Lancto CA, et al. Complete genome sequence of the apicomplexan, *Cryptosporidium parvum*. *Science* 2004;**304**: 441—5.
3. Xu P, Widmer G, Wang Y, Ozaki LS, Alves JM, Serrano MG, et al. The genome of *Cryptosporidium hominis*. *Nature* 2004;**431**: 1107—12.
4. Loftus B, Anderson I, Davies R, Alsmark UC, Samuelson J, Amedeo P, et al. The genome of the protist parasite *Entamoeba histolytica*. *Nature* 2005;**433**:865—8.
5. Berriman M, Ghedin E, Hertz-Fowler C, Blandin G, Renauld H, Bartholomeu DC, et al. The genome of the African trypanosome *Trypanosoma brucei*. *Science* 2005;**309**:416—22.
6. El-Sayed NM, Myler PJ, Bartholomeu DC, Nilsson D, Aggarwal G, Tran AN, et al. The genome sequence of *Trypanosoma cruzi*, etiologic agent of Chagas disease. *Science* 2005;**309**: 409—15.
7. Ivens AC, Peacock CS, Worthey EA, Murphy L, Aggarwal G, Berriman M, et al. The genome of the kinetoplastid parasite, *Leishmania major*. *Science* 2005;**309**:436—42.

Deborah F. Smith
Immunology and Infection Unit,
Department of Biology, University of York,
Heslington, York, YO10 5YW, UK
E-mail address: dfs501@york.ac.uk

6 October 2005